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(54) Title: NUCLEOTIDE SEQUENCE ENCODING A 52 kDa Ro/SSA AUTOANTIGEN			
(57) Abstract <p>Complementary DNA encoding a 52 kDa form of a protein present in the human Ro/SSA ribonucleoprotein complex has been cloned. A lambda gt11 cDNA library made from human thymus mRNA was screened with serum from an SLE patient and two immunoreactive clones were isolated. These clones reacted with other patient sera which had anti-52 kDa Ro/SSA antibodies and with affinity purified anti-52 kDa Ro/SSA antibodies. Moreover, affinity purified antibodies eluted from fusion proteins of the isolated clones reacted only with the 52 kDa protein of lymphocytes in the Western blot. Ro/SSA RNAs were also precipitated with these affinity purified antibodies, further confirming that the clones encode a 52 kDa Ro/SSA antigen. The sequence differs from the previously reported 60 kDa Ro/SSA gene. Both the cDNA and the protein expressed therefrom, or portions of either, are useful as diagnostic agents in the identification of patients having autoantibodies and in the identification and analysis of the structural and functional properties of the autoantigen and for application in immunotherapeutic regimens.</p>			

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NUCLEOTIDE SEQUENCE ENCODING A 52 KDA RO/SSA AUTOANTIGEN**Background of the Invention**

The present invention is the nucleotide sequence encoding a 52 kDa Ro/SSA autoantigen found in some systemic lupus erythematosus and Sjogren's syndrome patients, the encoded protein and methods for use thereof in diagnostic and therapeutic applications.

Systemic lupus erythematosus (SLE) is similar to many other disorders in which autoantibodies are found and thought to be important in etiology and pathogenesis. SLE can be grouped with those diseases that commonly have autoantibodies present but for whom a central role of autoantibody in pathogenesis leading to clinical expression has yet to be fully established or accepted. Other such diseases include Sjogren's syndrome, rheumatoid arthritis, insulin-dependent diabetes mellitus, primary biliary cirrhosis, Wegener's granulomatosis, inflammatory bowel disease, polymyositis, dermatomyositis, scleroderma, and many others.

Typically, autoimmune diseases present with a wide array of symptoms and clinical signs. The production of circulating autoantibodies to ribonucleoprotein complexes (RNPs) is a unifying characteristic of some of the rheumatic autoimmune diseases. The most common antigens in SLE and closely related disorders include: Ro/SSA, La/SSB, nRNP and Sm. Initially, these antibodies were found using double immunodiffusion, but more recently sensitive solid phase assays have been developed to quantitate the autoantibodies. The Ro/SSA RNA-protein particle has been found to be a constituent of all human cells evaluated to date. Approximately half of Sjogren's syndrome and systemic lupus erythematosus (lupus) patients have anti-Ro/SSA precipitins. Approximately 75% of patients with subacute cutaneous lupus erythematosus or complement component C2 deficiency with SLE have anti-Ro/SSA precipitins, and virtually all patients with

C2 or C4 deficiency have elevated levels of anti-Ro/SSA when measured by ELISA. Over 80% of mothers of newborns with neonatal lupus dermatitis or complete congenital heart block have these autoantibodies. As many as 5% of patients with rheumatoid arthritis, polymyositis, and progressive systemic sclerosis have anti-Ro/SSA, as reported by R.M. Bernstein, et al., Mol. Biol. Med. 2:105-120 (1984); and J.B. Harley and K.K. Gaither, Autoantibodies. In Rheumatic Disease Clinics of North American: Systemic Lupus Erythematosus 14:1, 43-56 (1988).

It has also been shown that some normal individuals have low levels of anti-Ro/SSA, that some normal family members of SLE patients have anti-Ro/SSA, and that 1% of normal pregnant women, and 0.1% of a cohort of hospitalized patients have precipitating levels of this autoantibody (K.K. Gaither, et al., J. Clin. Invest. 79:841-846 (1987); T.J.A. Lehman, et al., J. Rheumatol. 11:644-647 (1987); M. Calmes and B.A. Bartholomew, J. Clin. Pathol. 38:73-75 (1985); P.J. Maddison, et al., J. Rheumatol. 5:407-411 (1978)). Even if the anti-Ro/SSA autoantibody is not pathogenic, the concentrations of anti-Ro/SSA autoantibody achieved by patients can be extraordinary, and is commonly higher than 1 mg/ml of specific anti-Ro/SSA immunoglobulin (K.K. Gaither and J.B. Harley, Prot. Biol. Fluids Proc. Colloq. 33:413-416 (1985); J.B. Harley, et al., Arthritis Rheum. 29:196-206 (1986)). The immune system derangement leading to this specific overproduction of anti-Ro/SSA is not apparent but is likely to reflect a fundamental mechanism related to the immunopathogenesis of the related diseases.

Ro/SSA has been referred to by several other names, including "SSA/Ro", "SS-A/Ro", "SS-A", "Ro", and "Ro(SSA)". Historically, the biochemical characterization of the Ro/SSA complex has centered

around a 60 kDa protein associated with one of four hY RNAs, ranging from 80 to 112 bases, although the antigenic reactivity of the complex appears to be independent of the RNA. The Ro/SSA family of proteins has now been shown to have several molecular forms which are operationally defined by the molecular weight of the antigen identified. As reviewed by Ben-Chetrit, et al., in J. Exp. Med. 167, 1560-1571 (1988), the protein components of Ro/SSA have been described as polypeptides having molecular masses ranging from 50 to 150 kiloDaltons (kD). A major form has an apparent molecular weight of 60 kDa. Recently, two additional proteins bound by anti-Ro/SSA sera have been identified by M.D. Rader, et al., J. Clin. Invest. 83:1556-1562 (1989), with molecular weights of 52 kDa and 54 kDa. Ben-Chetrit, et al., (1988) also report a 52 kDa protein. Chan, et al., reported at the Molecular and Cell Biology of Autoantibodies and Autoimmunity, First International Workshop, July 27-29 (1989), that they had cloned a gene encoding a 46 kDa protein reactive with antisera against a 52 kDa Ro/SSA protein that was distinct, based on sequence comparison, from the cDNA of 60 kDa Ro/SSA. Other groups have confidentially reported that they have isolated cDNA encoding a different 60 kDa protein, having a molecular weight predicted by sequence analysis of 48 kDa.

It is impossible to determine at this time how many different autoantigens are produced which form complexes with RNA and that are characteristic, or involved in the pathogenesis, of autoimmune disorders in humans, such as SLE and Sjogren's syndrome. The proteins may vary not only from patient to patient, but in cellular origin. For example, in nucleated cells, 60, 52 and perhaps 45 kDa forms of the Ro/SSA protein have been found using Western blot

analysis. Certain lupus patient sera contain antibodies which recognize only the 60 kDa form, others only the 52 kDa form, and others have antibodies which bind to both the 60 and 52 kDa forms. In red blood cells, 60 and 54 kDa proteins have been identified in Ro/SSA particles. It appears that these proteins can only be identified with any certainty by comparison of nucleotide and amino acid sequence comparison.

It is therefore an object of the present invention to provide cDNA encoding an autoantigen characterized by a molecular weight of approximately 52 kDa to which serum antibodies are produced by certain patients having autoimmune disorders.

It is a further object of the present invention to provide the cDNA and the protein encoded by the cDNA and methods for use thereof for diagnostic and therapeutic purposes.

Summary of the Invention

Complementary DNA encoding a 52 kDa form of a protein present in the human Ro/SSA ribonucleoprotein complex has been cloned. A lambda gt11 cDNA library made from human thymocyte mRNA was screened with serum from a SLE patient and two immunoreactive clones were isolated. These clones reacted with other patient sera which had anti-52 kDa Ro/SSA antibodies and with affinity purified anti-52 kDa Ro/SSA antibodies. Moreover, affinity purified antibodies eluted from fusion proteins of the isolated clones reacted only with the 52 kDa protein of lymphocytes in the Western blot. Ro/SSA RNAs were also precipitated with these affinity purified antibodies, further confirming that the clones encode a 52 kDa Ro/SSA antigen. The sequence differs from the previously reported 60 kDa Ro/SSA gene.

Both the cDNA and the protein expressed therefrom, or portions of either, are useful as diagnostic and therapeutic agents in the identification and treatment of patients having autoantibodies and in the identification and analysis of the structural and functional properties of autoantigens reactive with antibodies to the 52 kDa protein. The cDNA is also useful in the isolation of nucleic acids encoding related proteins. The related proteins can be expressed from these sequences and are also useful as diagnostic and therapeutic agents.

Brief Description of the Drawing

Figure 1 shows the cDNA sequence for the Ro/SSA 52 kDa protein.

Figure 2 shows the predicted amino acid sequence of this gene. The predicted size of the polypeptide encoded by this sequence is 54,108 daltons.

Detailed Description of the Invention

cDNA encoding a protein having a molecular weight of 52 kDa based on SDS-PAGE and immunological identification in Western blots and a predicted molecular weight of 54,108 daltons has been cloned. The cDNA sequence is shown in Figure 1 and the encoded amino acid sequence is shown in Figure 2. The sequence is distinct from any published sequence, including that for two different sequences which may encode the 60 kDa Ro/SSA protein, providing further support for the heterogeneity of this group of proteins. There is similarity between the amino-terminal portions of this predicted protein and the amino-termini of both the mouse rpt-1 protein, a T cell regulatory protein, and the predicted human ret/rfp protein. The level of identity between the

amino terminal portion of this cloned protein and the latter two sequences are 48 and 43%, respectively. This area in the three proteins include zinc finger motifs. Further similarity is found between the carboxy-terminal ends of the predicted protein for this 52 kDa Ro/SSA molecule and the human rfp protein (51% identity), suggesting that the gene encoding this Ro/SSA protein may be a member of a larger gene family. It is also possible that polymorphisms of this gene will be identified, i.e. genetic differences in the nucleotide sequence of this gene may exist in humans, perhaps between patients and healthy controls, or in a subset of patients. These polymorphic genes and their protein products (and any of their modified forms) can be identified and isolated using either the disclosed cDNA sequence or protein expressed from the sequence, using techniques known to those skilled in the art, such as those described by Maniatis, et al., Molecular Cloning. A Laboratory Manual (Cold Spring Harbor Laboratory, NY 1982). For example, the related sequences can be identified and isolated by hybridization under standard conditions to a probe having a sequence shown in Figure 1 (65°C in the absence of formamide, with unbound probe removed by washing with decreasing concentrations of from 1 to 2 x SSPE to 0.5 x SSPE).

Referring to Figure 1, the first methionine residue is encoded by an ATG codon beginning at position 39. A stop codon (TGA) is found at position 1463. A putative poly-adenylation recognition site (AATAAA) is located at position 1827. This normally occurs approximately 20 bases upstream of poly-A sequences on eukaryotic mRNAs. Thus a 414 base 3' untranslated region occurs on this molecule. The enzyme EcoRI, which has a recognition sequence

GAATTC occurring at the beginning and end of this sequence, cleaves this cDNA just short of the poly-A sequence.

As shown in Figure 2, this predicted molecular weight of the encoded protein is slightly larger than the experimentally determined size of the 52 kilodalton protein. Post-translational processing or unusual secondary structure of this gene product is hypothesized to result in the 52 kDa band detected on Western blots.

Protein can be expressed from the cDNA using standard techniques for expression *in vitro* in cell free translation systems, in bacteria, yeast, and animal cells, including insect, amphibian, avian, and mammalian cells, as well as genetically engineered animals. The techniques are known to those skilled in the art. Reagents, including expression vectors and cell lines, for use in these methods are commercially available.

It is understood that specific cDNA sequences can be modified by those skilled in the art, for example, by labelling, fusion with regulatory sequences, insertion into expression vectors, site-directed mutagenesis and substitution or deletion of nucleotides encoding specific amino acids, without departing from the scope of the nucleotide and amino acid sequences of the present invention, and the methods for their use.

There are several embodiments of diagnostic reagents using the cDNA and protein expressed therefrom, in whole or in part, that can be used for diagnosis of autoimmune disorders or presence of autoantibodies. Antibodies to the protein obtained either from patients, immunized animals, or from antigen-specific monoclonal cell lines can be used to detect the respective antigen in cell extracts or serum and body fluids. These antibody assays include assays such as sandwich

ELISA assays, Western immunoblot, radioimmunoassays, and immunodiffusion assays. Techniques for preparing these reagents and methods for use thereof are known to those skilled in the art.

Expressed protein can also be used to immunize animals to generate polyclonal antisera and/or monoclonal antibodies. These, as well as patient autoantibodies, can be used to analyze structure and function of this protein. Protease cleaved fragments of the expressed proteins, or synthetically produced oligopeptides generated from the predicted sequence can be isolated and used to detect autoantibodies, as well as determine the epitope structure of the autoantigens. The expressed protein, or modifications thereof as described above, can be used to purify antibodies from different patients in order to study the heterogeneity of this autoimmune response, and if such heterogeneity is found, to appreciate the relationship between such heterogeneity and disease differences in these patients.

Nucleotide or amino acid probes can be prepared based on the sequence in Figure 1. These are labelled using dyes, or enzymatic, fluorescent, chemiluminescent, or radioactive labels which are commercially available. These probes can be used to detect the expression of this gene or related sequences in cells, tissue samples, or in *in vitro* reagents, as well as to screen sera or tissue samples from humans suspected of having autoantibody. For example, the appropriate nucleic acid sequences (or their complementary nucleic acid) could be used for *in situ* hybridization as a method to detect expression of genes encoding the antigen for the autoantibodies in specific tissues or peripheral blood cells. Levels of gene expression can be quantitated in patients and compared to healthy controls, or can be compared between different tissues. Differential tissue expression, coupled with data on

tissue pathology and detection of anti-52 kDa antibodies in these tissues, may be used to analyze the relation between antibody binding *in vivo* and disease pathogenesis. Nucleic acid primers could also be prepared which, with reverse transcriptase or DNA polymerase and the polymerase chain reaction, could be used to expand prospective antigenic sequences. Polymorphisms of this gene may be detected following restriction enzyme digestion of cellular DNA with subsequent electrophoresis and transfer of DNA to a membrane. Products of alleles to the sequence reported in Figure 1 may bind to patient autoantibodies with different affinities or may cross-react with epitopes present on other particles. The cDNA probe can also be used to clone the 52 kDa Ro/SSA gene from chromosomal DNA from which questions regarding differential splicing of exons and gene regulation can be addressed. Alterations of the DNA by site-directed mutagenesis may be used to determine functional regions including those which bind to hY RNAs.

Therapeutic applications of the cDNA and proteins expressed therefrom include using the expressed protein to adsorb circulating patient autoantibodies. These proteins, fragments of protein, or oligopeptides derived from the predicted sequence can be bound to solid phase particles over which the patient plasma may pass during plasmapheresis and extracorporeal immunoadsorption, thus reducing anti-Ro/SSA antibody levels before the remaining plasma is returned to the patient. If public idiotypes are found on anti-52 kDa Ro/SSA autoantibodies from different patients, appropriate fragments of these antibodies can be used to generate anti-idiotypic antibodies. The latter antibodies may be used either to block binding of anti-52 kDa antibodies to the native Ro/SSA particle *in vivo*, or to replace the anti-Ro/SSA

molecules discussed above for treatment involving plasmapheresis and extracorporeal immunoadsorption.

The present invention will be further described with reference to the following description of the isolation and characterization of the 52 kDa Ro/SSA protein cDNA.

Absorption of *E. coli* Antibodies:

Human sera from patients and controls were adsorbed against *E. coli* following lysis with the bacteriophage vector lambda gt11 to deplete naturally occurring anti *E. coli* antibodies from the sera. Briefly, five petri dishes with 30-50,000 plaque forming units (pfu) were plated with *E. coli* strain Y1090 cells on LB agar and grown for 4 hours at 42°C. Each dish was overlaid with a single nitrocellulose filter for 3 hours on one side and 2 hours on the other side at 37°C. Filters were removed and washed in TBST (50 mM Tris-HCl, pH 8.0; 150 mM NaCl; and 0.5% Tween-20). Filters were then sequentially incubated for one hour each at room temperature with human serum diluted 1:100 in TBST containing 3% bovine serum albumin and 0.02% sodium azide. The success of these adsorptions was monitored by removing a small piece of each filter following the serum incubation, blocking with 5% nonfat dry milk in TBST, washing, and incubating with an alkaline phosphatase conjugated, goat anti-human IgG antisera (Sigma Chemical Co., St. Louis; 1:1000 dilution in TBST containing 5% nonfat dry milk). These filter pieces were then reacted with nitro blue tetrazolium (NBT) and 5-bromo-4-chloro-3-indolylphosphate (BCIP) in alkaline phosphatase buffer (100 mM Tris-HCl, pH 9.5; 100 mM NaCl; 5 mM MgCl₂) according to the ProtoBlot System (Promega Corp., Madison).

Screening a human cDNA library:

A human thymocyte cDNA library was purchased from Clontech Laboratories (Palo Alto, CA.). 30,000 pfus per petri dish were plated with *E. coli* Y1090 cells on LB agar and incubated at 42°C for 4 hours. The partially lysed *E. coli* lawn was then overlaid for 3 hours at 37°C with a nitrocellulose membrane which had previously been soaked in 10 mM isopropylthio- β -galactoside (IPTG). Filters were removed, washed in TBST, incubated with an *E. coli* adsorbed patient serum containing antibodies to the 52 kDa Ro/SSA protein, and screened using the alkaline phosphatase method described above. Blue colored positive plaques were plaque purified using the same patient serum. Two clones, FI18.1 and FI19.3, were retested and found to react with sera from a panel of lupus patients which contained autoantibodies which react with the 52 kDa Ro/SSA protein as detected by Western blot assay. IPTG-induced proteins from these clones do not react with antibodies in sera from healthy controls nor patients with autoantibodies to the 60 kDa but not the 52 kDa Ro/SSA polypeptide.

Affinity Purification of Patient Antibodies:

Antibodies were affinity purified from two sources: (1) Western blotted polyacrylamide gels of human lymphocyte or HeLa cell extracts, and (2) nitrocellulose blots of IPTG-induced proteins from the plaque purified clones FI18.1 and FI19.3. For the first method, human cells were lysed by sonication in water and centrifuged to remove debris. Supernatants were reduced, heat denatured, and subjected to electrophoresis on a 10% polyacrylamide gel. Proteins were electrophoretically transferred to nitrocellulose membranes using the method of Towbin, H. T. Staehelin, and J. Gordon Proc. Natl. Acad. Sci. USA 76:4350-4354 (1979), from which a small strip was removed,

soaked in TBST containing 5% nonfat dry milk, and allowed to react with serum from a patient containing anti-52 kDa Ro/SSA autoantibodies. The filter piece was treated with alkaline phosphatase conjugated anti-human antisera and developed with NBT and BCIP as described above to localize the section of the membrane which contained the Ro/SSA 52 kDa proteins. The corresponding section of the remainder of the membrane was excised and incubated with patient serum for 30 minutes at 37°C. Following five TBST washes, bound antibodies were eluted using a modification of a method by Krohne, G., R. Stick, J.A. Kleinschmidt, R. Moll, W.W. Frankie, and P. Hausen J. Cell. Biol. 94:749-754 (1982). The membrane was incubated with patient serum for 30 minutes at 37°C, and the bound antibodies were eluted with 3 M sodium, rather than potassium, thiocyanate. The elution process was repeated five times and the resulting solution was concentrated approximately 50-fold using a Centriprep 30 concentrator (Amicon Division, W.R. Grace, Danvers, MA). Antibodies which bound to proteins produced in IPTG-induced plaque purified bacteriophage clones FI18.1 or FI19.3, or in wild type lambda gt11 as a control, were eluted in an identical manner from nitrocellulose blots.

Affinity purified antibodies isolated from Western blots of human lymphocyte or HeLa cell extracts were tested for their ability to bind to IPTG-induced proteins in clones FI18.1 and FI19.3, and in wild type lambda gt11 transfected *E. coli* cells. Affinity purified antibodies isolated from IPTG-induced proteins of these bacteriophage clones were used to determine their binding specificity to Western blots of human lymphocyte extracts using the method of Towbin, et al. (1979). The use of affinity purified antibodies in such assays was identical to that described for patient serum above, except that the affinity purified

antibodies were used undiluted. Antibodies eluted from proteins from IPTG-induced clones FI18.1 and FI19.3, but not IPTG-induced lambda gt11 transfected *E. coli* cells, bound only to a 52 kDa protein in Western blots. Affinity purified antibody from the 52 kDa region of Western blotted lymphocyte extracts bound to IPTG-induced proteins of clones FI18.1 and FI19.3, and not IPTG-induced proteins of lambda gt11 transfected *E. coli*.

Immunoprecipitations of Ro/SSA Proteins and hY RNAs:

Affinity purified antibodies isolated from IPTG-induced proteins of clone FI18.1 or FI19.3 were used to immunoprecipitate nucleic acids from HeLa cells which are bound to Ro/SSA proteins using the technique of Forman, M.S., M. Nakamura, T. Mimori, C. Gelpi, and J.A. Hardin *Arthritis Rheum.* 28:1356-1361 (1985). These antibodies were bound to Staphylococcal protein-A-coated Sepharose™ CL-4B beads (Pharmacia, Piscataway, NJ). HeLa cells were lysed by sonication in the presence of 0.05% NP-40 and mixed with these beads. Following washing of the beads, bound material was eluted with 0.3 M sodium acetate and 1% SDS, and subjected to phenol/chloroform extraction. Ethanol precipitated nucleic acids were dissolved in electrophoresis sample buffer and subjected to polyacrylamide gel electrophoresis in the presence of 7 M urea, and finally were silver stained. HY RNAs were identified using affinity purified antibodies from these clones, but not from IPTG-induced lambda gt11 transfected *E. coli*.

Characterization of DNA inserts in clones FI18.1 and FI19.3:

DNA was extracted from the bacteriophage clones, digested with the restriction enzyme *EcoRI* and electrophoresed in both agarose and polyacrylamide gels. Staining with ethidium bromide revealed that

both clones contained a single 1.8 kilobase insert. DNA from each clone was subjected to electrophoresis in 0.8% agarose gels and transferred to nylon membranes (Amersham, Arlington Heights, IL) by the method of Southern, E.M. J. Mol. Biol. 98:503-517 (1978).

Isolated inserts were radioactively labeled with α -³²P-dCTP using random hexamer primers by the procedures of Feinberg, A.P., and B. Vogelstein Anal. Biochem. 132:6-13 (1983) and Feinberg, A.P., and B. Vogelstein Anal. Biochem. 137:266-267 (1984), and hybridized to nylon membranes to analyze their sequence similarity in cross-hybridization studies. Following hybridization, the resulting membranes were washed under high stringency with 0.1 x SSPE (15 mM NaCl, 1 mM NaH₂PO₄, 0.1 mM EDTA, pH 7.0) and 0.1% SDS at 65°C. Hybridization was detected by autoradiography. Cross-hybridization of inserts of clones FI18.1 and FI19.3 was detected.

The *Eco*RI inserts from each bacteriophage clone were purified following electrophoresis through preparative 5% N,N'-bis-acrylylcystamine cross-linked polyacrylamide gels (Bio-Rad Laboratories, Richmond, CA), reduction in 2-mercaptoethanol, and DEAE ion-exchange chromatography. The resulting fragments were subcloned into an *Eco*RI digested M13mp19 bacteriophage vector, as described by Yanisch-Perron, C., J. Vieira, and J. Messing Gene 33:103-119 (1985). Additional DNA from clone FI18.1 was digested with other restriction enzymes chosen for their ability to produce DNA fragments which could be directly subcloned into the multiple cloning sites of M13mp19. Following ligation of these inserts to the vectors with T4 DNA ligase (Bethesda Research Laboratories, Gaithersburg, MD), DNA was transformed in *E. coli* strain JM103. Single stranded DNA from M13 subclones was prepared by the method of Sanger, F.,

S. Nicklen, and A.R. Coulson Proc. Natl. Acad. Sci. USA 74:5463-5467 (1977), and subjected to nucleotide sequencing using the dideoxy chain-termination method of Sanger, F., A.R. Coulson, B.G. Barrell, A.J.H. Smith, and B.A. Roe J. Mol. Biol. 143:161-178 (1980) and T7 DNA polymerase, as reported by Tabor, S., and C.C. Richardson. Proc. Natl. Acad. Sci. USA 84:4767-4771 (1987) (U.S. Biochemical Corp., Cleveland, OH). Additional nucleotide sequence was determined from deletion subclones which were produced using the exonuclease activity of T4 DNA polymerase from M13 phage clones containing large inserts, using the technique of Dale, R.M.K., B.A. McClure, and J.P. Houchins Plasmid 13:31-40 (1985). The resulting nucleotide sequence of this cDNA molecule is shown in Figure 1. Computer analysis of nucleotide sequences were performed using the Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin, described by Devereux, J., P. Haeberli, and O. Smithies Nucl. Acids Res. 12:387-395 (1984), and programs written for use on the IBM PC, including modification of those described by Schwindinger, W.F., and J.R. Warner Nucl. Acids Res. 12:601-604 (1984).

Methods for expression of large quantities of protein from the cDNA.
Methods for production of recombinant proteins.

In bacteria.

The protein can be expressed following IPTG induction from the lambda gt11 cDNA clone, or subclones of this cDNA in plasmids, or a portion thereof, or as modified using standard techniques, as described above.

In human or animals cell culture.

The protein can also be expressed from the cDNA, or a portion thereof, or as modified using standard techniques, following subcloning of the cDNA into a eukaryotic expression vector containing well characterized viral promoters and enhancers such as SV40 regulatory regions (Chu, G. and P.A. Sharp, Gene 13:197-202 (1981); the bovine papilloma virus (Howley, P.M., N. Sarver, and M.F. Law, Methods Enzymol. 101:357-402 (1983); or other expression vectors. These recombinant molecules can then be introduced into appropriate eukaryotic cells using the protoplast fusion technique (Schaffner, W., Proc. Natl. Acad. Sci. USA 77:2163-2167 (1986); Sadri-Goldin, R.M., et al., Methods Enzymol. 101:402-411 (1982)), CaPO₄ precipitation (Graham, F.L. and A.J. van der Eb Virology 52:456-457 (1973)), or other known methods. These recombinant molecules existing as either episomes, or as single or concatemeric copies integrated into chromosomal DNA can form stable transformed cells lines for expression of cDNA encoded proteins.

Following lysis of transfected bacterial or eukaryotic cells, the 52 kDa Ro/SSA protein can be purified with known methods including ion-exchange chromatography. Alternatively, the patent may be secreted from such cells depending on the host/vector system or modifications to the cDNA, and the resulting protein can be purified from cellular supernatants. The purity can be monitored by SDS-PAGE and immunodetection assays such as ELISA assays, radioimmunoassays, or Western blots.

Methods of production of antibodies to the recombinant proteins.

Polyclonal antisera produced by immunization of animals.

Animals can be immunized using standard techniques with the purified protein expressed from the cloned cDNA in order to produce polyclonal sera. Alternatively, monoclonal antibodies can be produced as follows, or using other methods also known to those skilled in the art.

Monoclonal antibodies produced by hybridomas.

BALB/c mice are injected intraperitoneally with 50-100 μ g of purified protein in complete Freund's adjuvant. The mice are again immunized after 3 weeks with the protein emulsified in incomplete Freund's adjuvant and after 6 weeks with the protein in TBS (0.1 M NaCl 0.02 M Tris-HCl pH 7.5). Four days later, spleen cells are fused with the mouse myeloma cell line P3X63AG8-653 using 35% polyethylene glycol 1450, using standard techniques, as described by Laurell, M., K. Ikeda, S. Lindgren, J. Stenflo, FEBS Letters 191, 75-81 (1985); Wakabayashi, K., Y. Sakata, N. Aoki, J. Biol. Chem. 261, 11097-11105 (1986); Borrebaeck, C.A.K., M.E. Etzler, J. Biol. Chem. 256, 4723-4725 (1981); Kohler, G., C. Milstein, Nature 256, 495-497 (1975).

Cells are grown in HAT medium to select for hybridomas. After four weeks, supernatants from fused cells are screened for antibody production by solid-phase enzyme-linked immunoadsorbent assay in the presence and absence of 5 mM Ca^{2+} .

Positive clones of interest, as determined on the basis of reactivity with antigen, are recloned at least two times by limiting dilution onto murine peritoneal lavage feeder cells.

A BALB/c mouse is initially primed with pristane to induce ascites fluid production and, 14 days later, injected intraperitoneally with 0.1 ml of 10 mg/ml cyclophosphamide in order to immunocompromise the animal. Seventy-four hours later, $3-6 \times 10^6$ cells are injected intraperitoneally. After 7-10 days, ascites fluid is collected and monoclonal antibodies purified from ascites fluid. Antibody is normally present at 8-15 mg antibody/ml ascites fluid. Two different methods can be used to purify the antibody: (1) NH_4SO_4 fractionation followed by QAE-Sephadex chromatography; or (2) affinity chromatography on antigen bound Affi-Gel™ 10.

Alternatively, selected hybridomas can be propagated *in vitro* in laboratory culture vessels from which the monoclonal antibodies against the selected antigen can be harvested by decantation and purified as described for the ascites fluid. The antigen affinity resin can also be used to isolate the monoclonal antibodies from hybridoma tissue culture supernatants. The material is directly applied to the column. The antibody concentration in an exponentially growing culture is approximately 25 $\mu\text{g}/\text{ml}$.

Xenogeneic Antibodies Produced In Severe Combined Immunodeficient Mice.

Adult retired breeder mice C.B-17 SCID (homozygous for SCID mutation) are obtained from the Fox Chase Cancer Institute and bred and maintained in a sterile environment. At 24 weeks of age or older, mice are removed from the sterile environment and injected with human peripheral blood mononuclear cells, using the method of Mosier, D.E., R.J. Galizia, S.M. Baird, D.B. Wilson *Nature* 335, 256-259 (1988). Mice are subsequently fed standard non-sterile mouse chow and

kept in isolation laminar flow cubicles (BioClean, Inc.). SCID mice are bled by tail vein.

Human peripheral blood mononuclear cells are obtained from patients having autoantibodies. Approximately 150 ml of blood is withdrawn into a heparinized container (preservative-free) and mononuclear cells separated by low speed density centrifugation (Histopak, Sigma Chemical Co., St. Louis, MO). Viability is determined by exclusion of trypan blue. Various numbers ($\times 10^6$) of isolated human mononuclear cells are injected intraperitoneally.

Enzyme linked immunosorbent assays (ELISA), performed using established techniques, as described by Gaither and Harley, Protides Biol. Fluids Proc. Colloq. 33, 413 (1985), are used to screen for the production of human IgG and specific autoantibodies. To screen for human IgG production, 96 well microtiter plates are coated with mouse serum at limiting dilutions. They are subsequently washed, blocked and goat anti-human IgG (gamma chain specific) alkaline phosphatase conjugate (Sigma Chemical Co., St. Louis, MO) added. After overnight incubation, microtiter plates are washed, substrate added and optical density readings taken on an ELISA reader (Beckman Instruments).

Engrafted mouse sera are screened for autoantibodies using a standard anti-Ro/SSA ELISA and highly purified Ro/SSA. Engrafted mouse sera is analyzed for anti-nuclear antibodies on Hep-2 cells using a NOVA Lite ANA (INOVA DIAGNOSTICS, Inc., San Diego, CA). Serum samples are diluted and 50-75 μ l applied to each substrate slide. After 30 min incubation in a moist chamber at room temperature, the slides are thoroughly washed with PBS. Goat anti-human IgG gamma chain specific FITC conjugate (Sigma Chemical Co., St. Louis, MO) is

added at 1:7500 dilution and incubated for 30 min at room temperature. Slides are subsequently washed with PBS and immunofluorescent staining visualized under a fluorescence microscope.

Modifications and variations of the cDNA and protein expressed therefrom, and methods for use thereof, will be obvious to those skilled in the art from the foregoing detailed description of the invention. Such modifications and variations are intended to come within the scope of the appended claims.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Oklahoma Medical, Research Found
- (ii) TITLE OF INVENTION: Nucleotide Sequence Encoding a 52 kDa
Ro/SSA Autoantigen
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Patrea L. Pabst
(B) STREET: Kilpatrick & Cody, 100 Peachtree St., Suite
3100
(C) CITY: Atlanta
(D) STATE: Georgia
(E) COUNTRY: U.S.A.
(F) ZIP: 30303
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 07-MAY-1991
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/520,270
(B) FILING DATE: 07-MAY-1990
- (viii) ATTORNEY/AGENT INFORMATION:

-22-

- (A) NAME: Pabst, Patrea L.
- (B) REGISTRATION NUMBER: 31,284
- (C) REFERENCE/DOCKET NUMBER: OMRF118

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 404/572-6508
- (B) TELEFAX: 404/562-6555
- (C) TELEX: 54-2307

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: human thymocyte
- (B) CLONE: FI18.1 and FI19.3

(x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: US 07/520,270 u
- (I) FILING DATE: 07-MAY-1990

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGC AACTGTCTGT TTAACGGCAC ACTTGACAAT GGCTTCAGCA GCACGCTTGA	60
CAATGATGTG GGAGGAGGTC ACATGCCCTA TCTGCCTGGA CCCCCTCGTG GAGCCTGTGA	120
GCATCGAGTG TGGCCACAGC TTCTGCCAGG AATGCATCTC TCAGGTTGGG AAAGGTGGGG	180
GCAGCGTCTG TCCTGTGTGC CGGCAGCGCT TTCTGCTCAA GAATCTCCGG CCCAATCGAC	240
AGCTAGCCAA CATGGTGAAC AACCTTAAAG AAATCAGCCA GGAGGCCAGA GAGGGCACAC	300
AGGGGGAACG GTGTGCAGTG CATGGAGAGA GACTTCACTT GTTCTGTGAG AAAGATGSGA	360
AGGCCCTTTG CTGGGTATGT G'CCAGTCTC GGAACACCG TGACCACGCC ATGGTCCCTC	420
TTGAGGAGGC TGCACAGGAG TACCAGGAGA AGCTCCAGGT GGCATTAGGG GAACTGAGAA	480
GAAAGCAGGA GTTGGCTGAG AAGTTGGAAG TGGAAATTGC AATAAGAGA GCAGACTGGA	540
AGAAAACAGT GGAACACAG AAATCTAGGA TTCACGCAGA GTTTGTGCAG CAAAAAAACT	600
TCCTGTTTGA AGAAGAACAG AGGCAGCTGC AGGAGCTGGA GAAGGATGAG AGGGAGCAGC	660
TGAGAATCCT GGGGGAGAAA GAGGCCAAGC TGGCCCAGCA GAGCCAGGCC CTACAGGAGC	720
TCATCTCAGA GCTAGATCGA AGGTGCCACA GCTCAGCACT GGAAC'GTCTG CAGGAGGTGA	780
GAATTGTCCT GGAAGGAGT GAGTCTCTGGA ACCTGAAGGA CCTGGATATT ACCTCTCCAG	840
AACTCAGGAG TGTGTGCCAT GTGCCAGGGC TGAAGAAGAT GCTGAGGACA TGTGCRGTCC	900
ACATCACTCT GGATCCAGAC ACAGCCAATC CGTGGCTGAT ACTTTCAGAA GATCGGAGAC	960
AAGTGAGGCT TGGAGACACC CAGCACAGCA TACCTGGAAA TGAAGAGAGA TTTGATAGTT	1020
ATCCTATGGT CCTGGGTGCC CAGCACTTTC ACTCTGAAA ACATTACTGG GAGGTAGATG	1080

1140 TGACAGGAAA GGAGGCCCTGG GACCTGGGTG TCTGCAGAGA CTCTGTGGCG AGGAAGGGGC
1200 ACTTTTGTCT TAGTTCCCAAG AGTGGCTTCT GGACAATTGG GTTGTGGAAC AAACAAAAAT
1260 ATGAGGCTGG CACCTACCCC CAGACTCCCC TCCACCTTCA GGTGCCTCCA TGCCAAGTTG
1320 GGAATTTTCCT GGACTATGAG GCTGGCATGG TCTCCTTCTA CAACATCACT GACCATGGCT
1380 CCGTCATCTA CTCCTTCTCT GAATGTGCCT TTACAGGACC TCTGCGGCCC TTCTTCAGTC
1440 CTGGTTTCAA TGATGGAGGA AAAAACACAG CCCCTCTAAC CCTCTGTCCA CTGAATATTG
1500 GATCACAAGG ATCCACTGAC TATTGATGGC TTTCTCTGGA CACTGCCACT CTCCCCATTG
1560 GCACCGCTTC TCAGCCACAA ACCCTGCCCTC TTTTCCCAT GAACTCTGAA CCACCTTTGT
1620 CTCTGCAGAG GCATCCGGAT CCCAGCAAGC GAGCTTTAGC AGGGAAGTCA CTTCAACCATC
1680 AACATTCTG CCCCAGATGG CTTTGTGATT CCCTCCAGTG AAGCAGCCTC CTTATATGTG
1740 GCCCRAACTC ATCTTGATCA ACCAAAAACA TGTTTCTGCC TTCTTTATGG GACTTAAAGTT
1800 TTTTTTTTCT CCTCTCCATC TCTAGGATGT CGTCTTTGGT GAGATCTCTA TTATATCTTG
1843 TATGGTTTGC AAAAGGGCTT CCTAAAAATA AAAACCCGAA TTC

-25-

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homo sapiens

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: thymocyte
- (B) CLONE: FI18.1 and FI19.3

(x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: US 07/520,270 u
- (I) FILING DATE: 07-MAY-1990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Ser	Ala	Ala	Arg	Leu	Thr	Met	Trp	Glu	Glu	Val	Thr	Cys	
1				5				10					15		
Pro	Ile	Cys	Leu	Asp	Pro	Phe	Val	Glu	Pro	Val	Ser	Ile	Glu	Cys	Gly
			20					25					30		
His	Ser	Phe	Cys	Gln	Glu	Cys	Ile	Ser	Gln	Val	Gly	Lys	Gly	Gly	Gly
			35					40					45		

Ser Val Cys Pro Val Cys Arg Gln Arg Phe Leu Leu Lys Asn Leu Arg
 50 55 60
 Pro Asn Arg Gln Leu Ala Asn Met Val Asn Asn Leu Lys Glu Ile Ser
 65 70 75 80
 Gln Glu Ala Arg Glu Gly Thr Gln Gly Glu Arg Cys Ala Val His Gly
 85 90 95
 Glu Arg Leu His Leu Phe Cys Glu Lys Asp Gly Lys Ala Leu Cys Trp
 100 105 110
 Val Cys Ala Gln Ser Arg Lys His Arg Asp His Ala Met Val Pro Leu
 115 120 125
 Glu Glu Ala Ala Gln Glu Tyr Gln Glu Lys Leu Gln Val Ala Leu Gly
 130 135 140
 Glu Leu Arg Arg Lys Gln Glu Leu Ala Glu Lys Leu Glu Asx Glu Ile
 145 150 155 160
 Ala Ile Lys Arg Ala Asp Trp Lys Lys Thr Val Glu Thr Gln Lys Ser
 165 170 175
 Arg Ile His Ala Glu Phe Val Gln Gln Lys Asn Phe Leu Val Glu Glu
 180 185 190
 Glu Gln Arg Gln Lys Gln Glu Leu Glu Lys Asp Glu Arg Glu Gln Leu
 195 200 205
 Arg Ile Leu Gly Glu Lys Glu Ala Lys Leu Ala Gln Gln Ser Gln Ala
 210 215 220
 Leu Gln Glu Leu Ile Ser Glu Leu Asp Arg Arg Cys His Ser Ser Ala
 225 230 235 240

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Leu Glu Leu Leu Gln Glu Val Ile Ile Val Leu Glu Arg Ser Glu Ser
245 250 255
Trp Asn Leu Lys Asp Leu Asp Ile Thr Ser Pro Glu Leu Arg Ser Val
260 265 270
Cys His Val Pro Gly Leu Lys Lys Met Leu Arg Thr Cys Ala Val His
275 280 285
Ile Thr Leu Asp Pro Asp Thr Ala Asn Pro Trp Leu Ile Leu Ser Glu
290 295 300
Asp Arg Arg Gln Val Arg Leu Gly Asp Thr Gln Gln Ser Ile Pro Gly
305 310 315 320
Asn Glu Glu Arg Phe Asp Ser Tyr Pro Met Val Leu Gly Ala Gln His
325 330 335
Phe His Ser Gly Lys His Tyr Trp Glu Val Asp Val Thr Gly Lys Glu
340 345 350
Ala Trp Asp Leu Gly Val Cys Arg Asp Ser Val Arg Arg Lys Gly His
355 360 365
Phe Leu Leu Ser Ser Lys Ser Gly Phe Trp Thr Ile Trp Leu Trp Asn
370 375 380
Lys Gln Lys Tyr Glu Ala Gly Thr Tyr Pro Gln Thr Pro Leu His Leu
385 390 395 400
Gln Val Pro Pro Cys Gln Val Gly Ile Phe Leu Asp Tyr Glu Ala Gly
405 410 415
Met Val Ser Phe Tyr Asn Ile Thr Asp His Gly Ser Leu Ile Tyr Ser
420 425 430

Phe Ser Glu Cys Ala Phe Thr Gly Pro Leu Arg Pro Phe Phe Ser Pro
435 440 445

Gly Phe Asn Asp Gly Gly Lys Asn Thr Ala Pro Leu Thr Leu Cys Pro
450 455 460

Leu Asn Ile Gly Ser Gln Gly Ser Thr Asp Tyr
465 470 475

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We claim:

1. Isolated nucleic acid sequence encoding a Ro/SSA autoantigen having a molecular weight by SDS-PAGE and Western blot of 52 kDa.
2. The sequence of claim 1 further comprising regulatory sequences selected from the non-protein coding sequences shown in Figure 1.
3. The sequence of claim 1 consisting essentially of the protein encoding sequence shown in Figure 1, after the first 38 bases.
4. The sequence of claim 2 comprising the entire sequence shown in Figure 1.
5. The sequence of claim 1 isolated from the human chromosome.
6. The sequence of claim 5 further comprising regulatory sequences for expression of the 52 kDa Ro/SSA autoantibody.
7. The sequence of claim 1 labelled with a detectable label.
8. The sequence of claim 1 hybridizing under standard conditions to the sequence shown in Figure 1, or portions thereof.
9. An isolated Ro/SSA autoantigen having a molecular weight by SDS-PAGE and Western blot of 52 kDa, or an antigenic portion thereof.
10. The protein of claim 9 having the sequence shown in Figure 2, or a portion thereof.
11. The protein of claim 9 produced by proteolytic cleavage of the protein expressed from the nucleotide sequence shown in Figure 1 or a sequence hybridizing under standard conditions to the nucleic acid shown in Figure 1.

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12. The protein of claim 9 produced synthetically based on the nucleotide sequence shown in Figure 1 or a sequence hybridizing under standard conditions to the nucleic acid shown in Figure 1.

13. The protein of claim 9 expressed by cells selected from the group consisting of bacteria, yeast, and animal cells.

14. The protein of claim 9 expressed by an *in vitro* cell free translation system.

15. The protein of claim 9 further comprising a detectable label.

16. The protein of claim 9 immobilized on a substrate not specifically binding antibodies.

17. A method for determining the presence of antibodies reactive with a Ro/SSA protein having a molecular weight by SDS-PAGE of 52 kDa comprising providing a reactive portion of an isolated 52 kDa Ro/SSA protein encoded by the protein encoding sequence shown in Figure 1 or a nucleic sequence hybridizing thereto under standard conditions.

18. The method of claim 17 wherein the protein is isolated by binding to antibodies reactive with a 52 kDa protein encoded by the sequence shown in Figure 1, or a sequence hybridizing thereto under standard conditions, and not reactive with other Ro/SSA proteins.

19. The method of claim 17 wherein the protein is expressed from an isolated nucleic sequence encoding a 52 kDa Ro/SSA autoantigen as shown in Figure 1, or a sequence hybridizing thereto under standard conditions, and said protein is chemically different from the naturally produced and isolated autoantigen.

20. The method of claim 17 wherein the protein is expressed in an *in vitro* cell free translation system.

21. The method of claim 17 wherein the protein is expressed in cells selected from the group consisting of bacteria, yeast, and animal cells.
22. The method of claim 17 wherein the reactive portion is a proteolytically cleaved fragment of the protein encoded by the sequence of Figure 1, or a nucleic sequence hybridizing thereto.
23. The method of claim 17 wherein the reactive portion is a chemically synthesized fragment of the protein encoded by the sequence of Figure 1, or a nucleic sequence hybridizing thereto.
24. The method of claim 17 wherein the presence of the anti-52 kDa Ro/SSA autoantibodies is determined by detecting a label bound to the protein.
25. The method of claim 17 wherein the presence of the anti-52 kDa Ro/SSA autoantibodies is determined by reacting a solution to be tested with the 52 kDa protein to bind anti-52 kDa protein antibodies to 52 kDa protein, removing the unbound materials, and detecting the presence of antibody bound protein.
26. The method of claim 25 wherein the antibody is in solution and the 52 kDa protein is immobilized on a substrate not specifically binding antibody.
27. The method of claim 25 wherein the antibody bound protein is separated by binding with a reagent specifically binding to antibody.
28. The method of claim 25 further comprising quantitating the amount of antibody bound protein.
29. A method for treating a patient comprising exposing the blood of a patient characterized by Ro/SSA autoantibodies to a 52 kDa protein to a protein selected from the group consisting of 52 kDa

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Ro/SSA protein, 52 kDa Ro/SSA fragments, 52 kDa Ro/SSA oligopeptides, and anti-idiotypic antibodies to 52 kDa Ro/SSA antibodies.

30. The method of claim 29 wherein the proteins are immobilized on a substrate in an apparatus for extracorporeal treatment of blood.

31. A protein binding with an antibody to a protein expressed by the nucleotide sequence shown in Figure 1 and hybridizing to the nucleotide sequence shown in Figure under standard conditions.

10 20 30 40 50 60
GAATTCGGGC AACTGCTGT TTAACGGCAC ACTTGACAAT GGCTTCAGCA GCACGCTTGA
70 80 90 100 110 120
CAATGATGTG GGAGGAGGTC ACATGCCCTA TCTGCCTGGA CCCCTTCGTG CAGCCTGTGA
130 140 150 160 170 180
GCATCGAGTG TGGCCACAGC TTCTGCCAGG AATGCATCTC TCAGGTTGGG AAAGGTGGGG
190 200 210 220 230 240
GCAGCGTCTG TCCTGTGTGC CGGCAGCGCT TTCTGCTCAA GAATCTCCGG CCCAATCGAC
250 260 270 280 290 300
AGCTAGCCAA CATGGTGAAC AACCTTAAAG AAATCAGCCA GGAGGCCAGA GAGGGCACAC
310 320 330 340 350 360
AGGGGGAACG GTGTGCAGTG CATGGAGAGA GACTTCACCT GTTCTGTGAG AAAGATGGGA
370 380 390 400 410 420
AGGCCCTTTG CTGGGTATGT GCCCAGTCTC GGAAACACCG TGACCACGCC ATGGTCCCTC
430 440 450 460 470 480
TTGAGGAGGC TGCACAGGAG TACCAGGAGA AGCTCCAGGT GGCATTAGGG GAACTGAGAA
490 500 510 520 530 540
GAAAGCAGGA GTTGGCTGAG AAGTTGGAAG TGGAAATTGC AATAAAGAGA GCAGACTGGA
550 560 570 580 590 600
AGAAAACAGT GGAAACACAG AAATCTAGGA TTCACGCAGA GTTTGTGCAG CAAAAAACT
610 620 630 640 650 660
TCCTGGTTGA AGAAGAACAG AGGCAGCTGC AGGAGCTGGA GAAGGATGAG AGGGAGCAGC
670 680 690 700 710 720
TGAGAATCCT GGGGGAGAAA GAGGCCAAGC TGGCCCAGCA GAGCCAGGCC CTACAGGAGC
730 740 750 760 770 780
TCATCTCAGA GCTAGATCGA AGGTGCCACA GCTCAGCACT GGAAGTCTG CAGGAGGTGA
790 800 810 820 830 840
TAATTGTCTT GGAAAGGAGT GAGTCCTGGA ACCTGAAGGA CCTGGATATT ACCTCTCCAG
850 860 870 880 890 900
AACTCAGGAG TGTGTGCCAT GTGCCAGGGC TGAAGAAGAT GCTGAGGACA TGTGCAGTCC
910 920 930 940 950 960
ACATCACTCT GGATCCAGAC ACAGCCAATC CGTGGCTGAT ACTTTCAGAA GATCGGAGAC
970 980 990 1,000 1,010 1,020
AAGTGAGGCT TGGAGACACC CAGCAGAGCA TACCTGGAAA TGAAGAGAGA TTTGATAGTT

FIGURE 1

1,030 1,040 1,050 1,060 1,070 1,080
ATCCTATGGT CCTGGGTGCC CAGCACTTTC ACTCTGGAAA ACATTACTGG GAGGTAGATG

1,090 1,100 1,110 1,120 1,130 1,140
TGACAGGAAA GGAGGCCTGG GACCTGGGTG TCTGCAGAGA CTCTGTGCCG AGGAAGGGGC

1,150 1,160 1,170 1,180 1,190 1,200
ACTTTTGGCT TAGTTCCAAG AGTGGCTTCT GGACAATTTC GTTGTGGAAC AAACAAAAT

1,210 1,220 1,230 1,240 1,250 1,260
ATGAGGCTGG CACCTACCCC CAGACTCCCC TCCACCTTCA GGTGCCTCCA TGCCAAGTTG

1,270 1,280 1,290 1,300 1,310 1,320
GGATTTTCCT GGACTATGAG GCTGGCATGG TCTCCTTCTA CAACATCACT GACCATGGCT

1,330 1,340 1,350 1,360 1,370 1,380
CCCTCATCTA CTCCTTCTCT GAATGTGCCT TTACAGGACC TCTGCGGCC TTCTTCAGTC

1,390 1,400 1,410 1,420 1,430 1,440
CTGGTTTCAA TGATGGAGGA AAAAACACAG CCCCTCTAAC CCTCTGTCCA CTGAATATTG

1,450 1,460 1,470 1,480 1,490 1,500
GATCACAAGG ATCCACTGAC TATTGATGGC TTTCTCTGGA CACTGCCACT CTCCCCATTG

1,510 1,520 1,530 1,540 1,550 1,560
GCACCGCTTC TCAGCCACAA ACCCTGCCTC TTTTCCCAT GAACCTGTAA CCACCTTTGT

1,570 1,580 1,590 1,600 1,610 1,620
CTCTGCAGAG GCATCCGGAT CCCAGCAAGC GAGCTTAGC AGGGAAGTCA CTTCAACATC

1,630 1,640 1,650 1,660 1,670 1,680
AACATTCTCG CCCAGATGG CTTTGTGATT CCCTCCAGTG AAGCAGCCTC CTTATATTG

1,690 1,700 1,710 1,720 1,730 1,740
GCCCAAATC ATCTTGATCA ACCAAAAACA TGTTTCTGCC TTCTTTATGG GACTTAAGTT

1,750 1,760 1,770 1,780 1,790 1,800
TTTTTTTCT CCTCTCCATC TCTAGGATGT CGTCTTTGGT GAGATCTCTA TTATATCTG

1,810 1,820 1,830 1,840 1,850
TATGTTTTCG AAAAGGGCTT CCTAAAAATA AAAACCCGAA TTC

FIGURE 1 CONTINUED

5 10 15 20 25 30
MASAA RL TMM WEEVT CPICL DPFVE PVSIE
35 40 45 50 55 60
CGHSF CQECI SQVGK GGGSV CPVCR QRFL
65 70 75 80 85 90
KNLRP NRQLA NMVNN LKEIS QEARE GTQGE
95 100 105 110 115 120
RCAVH GERLH LFCEK DGKAL CWVCA QSRKH
125 130 135 140 145 150
RDHAM VPLEE AAQEY QEK LQ VALGE LRRKQ
155 160 165 170 175 180
ELA EK LEVEI AIKRA DWKKT VETQK SRIHA
185 190 195 200 205 210
EFVQQ KNFLV EEEQR QLQEL EKDER EQLRI
215 220 225 230 235 240
LGEKE AKLAQ QS QAL QELIS ELDRR CHSSA
245 250 255 260 265 270
LELLQ EVIIV LERSE SWNLK DLDIT SPELR
275 280 285 290 295 300
SVCHV PGLKK MLRTC AVHIT LDPDT ANPWL
305 310 315 320 325 330
ILSED RRQVR LGDTQ QSI PG NEERF DSYPM
335 340 345 350 355 360
VLGAQ HFHSG KHYWE VDV TG KEAWD LGVCR
365 370 375 380 385 390
DSVRR KGHFL LSSKS GFWTI WLWNK QKYE A
395 400 405 410 415 420
GTYPQ TPLHL QVPPC QVGIF LDYEA GMVSF
425 430 435 440 445 450
YNITD HGS LI YSFSE CAFTG PLRPF FSPGF
455 460 465 470 475
NDGGK NTAPL TLCPL NIGSQ GSTDY

FIGURE 2

INTERNATIONAL SEARCH REPORT

International Application No. PCT/US91/03139

I. CLASSIFICATION OF SUBJECT MATTER of several classification symbols apply, indicate all *

According to International Patent Classification (IPC) or to both National Classification and IPC

IPC(5): C07 H 15/12

U.S. Cl.: 536/27

II. FIELDS SEARCHED

Minimum Documentation Searched *

Classification System	Classification Symbols
US	536/27

Documentation Searched other than Minimum Documentation
to the extent that such Documents are included in the Fields Searched *

Automated patent search system USPAT, commercial computer data banks SIN and DIALOG

III. DOCUMENTS CONSIDERED TO BE RELEVANT *

Category *	Citation of Document, ** with indication, where appropriate, of the relevant passages **	Relevant to Claim No. **
A	JOURNAL OF CLINICAL INVESTIGATIONS, VOLUME 83, NUMBER 4, ISSUED 1989, E. BEN-CHETRIT ET AL., "ISOLATION AND CHARACTERIZATION OF A COMPLEMENTARY DNA CLONE ENCODING THE 60-KD COMPONENT OF THE SS-A-RO RIBONUCLEOPROTEIN AUTOANTIGEN", PAGES 1284-1292; ABSTRACT ONLY.	1-28
A	WO, A, 89/09273 (UNIVERSITY OF TEXAS-SYS.) 10 MAY 1989; ABSTRACT ONLY.	1-28

- * Symbols:
- "A" document defining the general state of the art which is not considered to be of particular relevance
 - "E" earlier document but published on or after the international filing date
 - "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
 - "O" document referring to an oral disclosure, use, exhibition or other means
 - "P" document published prior to the international filing date but later than the priority date claimed

- ** Symbols:
- "X" document of particular relevance, the claimed invention cannot be considered novel or cannot be considered, to involve an inventive step
- "Y" document of particular relevance, the claimed invention cannot be considered to involve an inventive step when the document is combined with prior art documents or combinations, such combination being obvious to a person skilled in the art.
- "Z" document member of the state patent law.

IV. CERTIFICATION

Date of the Actual Completion of the International Search

03 July 1991

Date of Mailing of this International Search Report

19 AUG 1991

International Searching Authority

ISA/US

Signature of Authorized Officer

Bradley L. Sisson

FURTHER INFORMATION CONTINUED FROM THE SECOND SHEET

V. ☐ OBSERVATIONS WHERE CERTAIN CLAIMS WERE FOUND UNSEARCHABLE

This international search report has not been established in respect of certain claims under Article 17(2) (a) for the following reasons:

1. ☐ Claim numbers _____, because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claim numbers _____, because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out¹⁴, specifically:

3. ☐ Claim numbers _____, because they are dependent claims not drafted in accordance with the second and third sentences of PCT Rule 6.4(a).

VI. ☒ OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This International Searching Authority found multiple inventions in this international application as follows:

See attached sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims of the international application.
2. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims of the international application for which fees were paid, specifically claims:
3. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claim numbers:

1-8

telephone practice

4. ☐ As all searchable claims could be searched without effort justifying an additional fee, the International Searching Authority did not invite payment of any additional fee.

Remark on Protest

- ☐ The additional search fees were accompanied by applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

Detailed Reasons for Holding Lack of Unity of Invention:

- I. Claims 1-8, drawn to nucleic acids, classified in Class 536, subclass 27.
- II. Claims 9-28 and 31, drawn to proteins and their use in immunoassays, classified in Class 435, subclass 7.1.
- III. Claims 29-30, drawn to extracorporeal treatment, classified in Class 604, subclass 5.

Detailed Reasons for Holding Lack of Unity of Invention (Continued):

The claims of these three groups are drawn to distinct inventions which are not linked so as to form a single inventive concept. PCT Rule 13.1 and 13.2 do not provide for multiple products and methods.

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0
2
4